AMENDMENT TO THE CLAIMS:

This listing of claims will replace all prior listings of claims in the application:

LISTING OF CLAIMS:

1-234. (Cancelled)

235. (Currently Amended) A method for identifying a compound that putatively elicits or modulates human T1R3 on polypeptide-associated taste in a human subject based on its effect on T1R3 polypeptide activation comprising:

(1) screening one or more compounds in a functional assay that detects compounds which activate or which modulate (enhance or inhibit) the activation of a human T1R3 polypeptide by another compound wherein said T1R3 polypeptide is selected from the group consisting of:

(a) a ~~T1R1~~ T1R3 polypeptide having the amino acid sequence contained in SEQ. ID. NO: 4;

(b) a human T1R3 polypeptide that possesses at least 90% sequence identity to the polypeptide contained in SEQ. ID. NO: 4 and which human T1R3 specifically binds to a sweet ligand;

(c) a human T1R3 polypeptide which is encoded by a nucleic acid sequence that hybridizes to the T1R3 polypeptide coding region of the nucleic acid sequence contained in SEQ. ID. NO: 2, SEQ ID NO:3 or SEQ. ID. NO: 20 under stringent hybridization conditions ~~or a functional fragment which is encoded by a portion of said coding region which is at least 500 nucleotides in length;~~ which are incubation in 50% formamide, 5X SCC and 1% SDS at 42 degrees C and wash in 0.1% SDS at 65

degrees C and wherein said human T1R3 polypeptide specifically binds to a sweet ligand;

~~(d) a human T1R3 polypeptide that is a functional fragment of a T1R3 polypeptide according to (a) or (b);~~

(2) identifying compounds (i) that putatively elicit or modulate T1R3 polypeptide-associated taste based on their (a) activation or modulation (inhibition or enhancement) of the activation of a T1R3 polypeptide by another compound according to (a), (b), or (c), ~~or (d),~~ in said functional assay (1).

236. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide has the amino acid sequence contained in SEQ. ID. NO: 4.

237. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide has an amino acid sequence that possesses at least 90% sequence identity to the polypeptide contained in SEQ. ID. NO: 4.

238. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide has an amino acid sequence that possesses at least 95% sequence identity to the polypeptide contained in SEQ. ID. NO: 4.

239. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide has an amino acid sequence that possesses at least 96% sequence identity to the polypeptide contained in SEQ. ID. NO: 4.

240. (Previously Presented) The method of claim 237, wherein the T1R3 polypeptide possesses at least 97% sequence identity to the polypeptide contained in SEQ. ID. NO: 4.

241. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide has an amino acid sequence that possesses at least 97% sequence identity to the polypeptide contained in SEQ. ID. NO: 4.

242. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide has an amino acid sequence that possesses at least 98% sequence identity to the polypeptide contained in SEQ. ID. NO: 4.

243. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide has an amino acid sequence that possesses at least 99% sequence identity to the polypeptide contained in SEQ. ID. NO: 4.

244. (Currently Amended) The method of claim 235, wherein said T1R3 polypeptide is encoded by a nucleic acid sequence that hybridizes to the T1R3 coding region contained in SEQ. ID. NO: 2, 3, or 20 under stringent hybridization conditions.

245. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide comprises a functional fragment of the polypeptide contained in SEQ. ID. NO: 4.

246. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide is expressed by a cell.

247. (Previously Presented) The method of claim 235, wherein said cell is intact or permeabilized.

248. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide is comprised in a membrane extract.

249. (Previously Presented) The method of claim 245, wherein said T1R3 polypeptide is expressed on the surface of said cell.

250. (Previously Presented) The method of claim 246, wherein the cell is a prokaryotic cell.

251. (Previously Presented) The method of claim 246, wherein the cell is a eukaryotic cell.

252. (Previously Presented) The method of claim 251, wherein said cell is a yeast, insect, amphibian or mammalian cell.

253. (Previously Presented) The method of claim 252, wherein the cell is a CHO, HEK-293, COS or Xenopus oocyte.

254. (Previously Presented) The method of claims 246, wherein said cell further expresses a G protein.

255. (Previously Presented) The method of claim 254, wherein said G protein is $G_{\alpha 15}$, $G_{\alpha 16}$ or gustducin.

256. (Previously Presented) The method of claim 235, wherein said functional assay detects the effect of said compound on phosphorylation of said T1R3 polypeptide.

257. (Previously Presented) The method of claim 235, wherein the functional assay detects the effect of said compound on the dissociation of said T1R3 polypeptide and a G protein.

258. (Previously Presented) The method of claim 235, wherein the functional assay detects the effect of said compound on arrestin translocation.

259. (Previously Presented) The method of claim 235, wherein the functional assay detects the effect of said compound on second messengers.

260. (Previously Presented) The method of claim 235, wherein the functional assay detects the effect of said compound on signal transduction.

261. (Previously Presented) The method of claim 235, wherein the functional assay is a GTPγS assay.

262. (Previously Presented) The method of claim 261, wherein said functional assay is a transcriptional assay.

263. (Previously Presented) The method of claim 259, wherein said functional assay detects changes in cAMP, cGMP, or IP3.

264. (Previously Presented) The method of claims 235, wherein said functional assay detects whether said compound results in a detectable change in intracellular calcium.

265. (Previously Presented) The method of claim 264, which uses a calcium-sensitive dye.

266. (Previously Presented) The method of claim 235 which detects the effect of said compound on G protein activation of said T1R3 polypeptide.

267. (Previously Presented) The method of claim 266, wherein said G protein is $G_{\alpha 15}$, or $G_{\alpha 16}$ or gustducin.

268. (Previously Presented) The method of claim 235, wherein said T1R3 polypeptide in said functional assay is stably or transiently expressed by a cell.

269. (Previously Presented) The method of claim 235, wherein the functional assay detects changes in ionic polarization of a cell or membrane that expresses the T1R3 polypeptide.

270. (Previously Presented) The method of claim 269, wherein ion polarization is detected by a voltage-clamp or patch-clamp method.

271. (Previously Presented) The method of claim 235, wherein said functional assay comprises a radiolabeled ion flux assay or a fluorescence assay that detects T1R3 activity using a voltage-sensitive dye.

272. (Previously Presented) The method of claim 235, wherein said assay comprises a fluorescent polarization or FRET assay.

273. (Previously Presented) The method of claim 235, wherein said assay detects changes in adenylate cyclase activity.

274. (Previously Presented) The method of claim 235, wherein the functional assay detects change in ligand dependent coupling of said T1R3 polypeptide with a G protein.

275. (Previously Presented) The method of claim 273, wherein said G protein is $G_{\alpha 15}$, $G_{\alpha 16}$ or gustducin.

276. (Previously Presented) The method of claim 235, wherein said functional assay detects changes in intracellular cAMP or cGMP.

277. (Previously Presented) The method of claim 235, wherein said assay measures the effect of said compound on transmitter or hormone release.

278. (Previously Presented) The method of claim 235 wherein said functional assay detects the effect of said compound on the transcription of a gene of interest.

279. (Previously Presented) The method of claim 271, wherein said gene is a reporter selected from chloramphenicol acetyltransferase, luciferase, 3'-galactosidase and alkaline phosphatase.

280. (Previously Presented) The method of claim 235, wherein the functional assay is a high throughput assay.

281. (Previously Presented) The method of 280, wherein said functional assay screens a library of compounds.

282. (Previously Presented) The method of claim 281, wherein said library is a combinatorial chemical library.

283. (Previously Presented) The method of claim 283, wherein said library comprises at least 1000 compounds.

284. (Previously Presented) The method of claim 235, wherein the effect of said putative T1R3 taste modulator is assayed in vivo for its effect on T1R3 receptor polypeptide-associated taste.

285. (Previously Presented) The method of claim 284 which assays the effect of said compound on the taste of a particular compound.

286. (Previously Presented) The method of claim 284, wherein said assay detects the effect of said compound on sweet or umami taste.